1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,677

DATE: 09/06/2000
TIME: 11:01:37

Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

Does Not Comply
Corrected Diskette Needed

See pp. 2, 4, 6

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: BIRKELUND, Svend
CHRISTIANSEN, Gunna
HEBSGAARD PEDERSEN, Anna-Sofie
MYGIND, Per
KNUDSEN, Katrine
(ii) TITLE OF INVENTION: SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
(iii) NUMBER OF SEQUENCES: 30
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
(B) STREET: 624 Ninth Street, N.W., Suite 300
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
(vi) CURRENT APPLICATION DATA:
C--> (A) APPLICATION NUMBER: US/09/446,677
C--> (B) FILING DATE: 24-Mar-2000
C--> (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/DK98/00266
(B) FILING DATE: 19-JUN-1998
(A) APPLICATION NUMBER: DK 0744/97
(B) FILING DATE: 23-JUN-1997
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: COOPER, Iver P.
(B) REGISTRATION NUMBER: 28,005
(C) REFERENCE/DOCKET NUMBER: BIRKELUND=1
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-628-5197
(B) TELEFAX: 202-737-3528

ERRORED SEQUENCES

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2815 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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Input Set : A:\Birkell.txt
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Enter "hard return" here to correct.

506 (ii) MOLECULE TYPE: Genomic DNA
508 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 510 ATGAAATCGC AATTTTCCTG GTTAGTGCTC TCTTCGACAT TGGCATGTTT TACTAGTTGT 60 TCCACTGTTT TTGCTGCAAC TGCTGAAAAT ATA(
511 ACTAACACAG GCACCTATAC TCCTAAAAAT ACGACTACTG GAATAGACTA TACTCTGACA 180
512 GGAGATATAA CTCTGCAAAA CCTTGGGGAT TCGGCAGCTT TAACGAAGGG TTGTTTTTCT 240
513 GACACTACGG AATCTTTAAG CTTTGCCGGT AAGGGGTACT CACTTTCTTT TTTAAATATT 300
514 AAGTCTAGTG CTGAAGGCGC AGCACTTTCT GTTACAACTG ATAAAAATCT GTCGCTAACA 360
515 GGATTTTCGA GTCTTACTTT CTTAGCGGCC CCATCATCGG TAATCACAAC CCCCTCAGGA 420
516 AAAGGTGCAG TTAAATGTGG AGGGGATCTT ACATTTGATA ACAATGGAAC TATTTTATTT 480
517 AAACAAGATT ACTGTGAGGA AAATGGCGGA GCCATTTCTA CCAAGAATCT TTCTTTGAAA 540
518 AACAGCACGG GATCGATTTC TTTTGAAGGG AATAAATCGA GCGCAACAGG GAAAAAAGGT 600
519 GGGGCTATTT GTGCTACTGG TACTGTAGAT ATTACAAATA ATACGGCTCC TACCCTCTTC 660
520 TCGAACAATA TTGCTGAAGC TGCAGGTGGA GCTATAAATA GCACAGGAAA CTGTACAATT 720
521 ACAGGGAATA CGTCTCTTGT ATTTTCTGAA AATAGTGTGA CAGCGACCGC AGGAAATGGA 780
522 GGAGCTCTTT CTGGAGATGC CGATGTTACC ATATCTGGGA ATCAGAGTGT AACTTTCTCA 840
523 GGAAACCAAG CTGTAGCTAA TGGCGGAGCC ATTTATGCTA AGAAGCTTAC ACTGGCTTCC 900
524 GGGGGGGGGG GGGGTATCTC CTTTTCTAAC AATATAGTCC AAGGTACCAC TGCAGGTAAT 960
525 GGTGGAGCCA TTTCTATACT GGCAGCTGGA GAGTGTAGTC TTTCAGCAGA AGCAGGGGAC 1020
526 ATTACCTTCA ATGGGAATGC CATTGTTGCA ACTACACCAC AAACTACAAA AAGAAATTCT 1080
527 ATTGACATAG GATCTACTGC AAAGATCACG AATTTACGTG CAATATCTGG GCATAGCATC 1140
528 TTTTTCTACG ATCCGATTAC TGCTAATACG GCTGCGGATT CTACAGATAC TTTAAATCTC 1200
529 AATAAGGCTG ATGCAGGTAA TAGTACAGAT TATAGTGGGT CGATTGTTTT TTCTGGTGAA 1260
530 AAGCTCTCTG AAGATGAAGC AAAAGTTGCA GACAACCTCA CTTCTACGCT GAAGCAGCCT 1320
531 GTAACTCTAA CTGCAGGAAA TTTAGTACTT AAACGTGGTG TCACTCTCGA TACGAAAGGC 1380
532 TTTACTCAGA CCGCGGGTTC CTCTGTTATT ATGGATGCGG GCACAACGTT AAAAGCAAGT 1440
533 ACAGAGGAGG TCACTTTAAC AGGTCTTTCC ATTCCTGTAG ACTCTTTAGG CGAGGGTAAG 1500
534 AAAGTTGTAA TTGCTGCTTC TGCAGCAAGT AAAAATGTAG CCCTTAGTGG TCCGATTCTT 1560
535 CTTTTGGATA ACCAAGGGAA TGCTTATGAA AATCACGACT TAGGAAAAAC TCAAGACTTT 1620
536 TCATTTGTGC AGCTCTCTGC TCTGGGTACT GCAACAACTA CAGATGTTCC AGCGGTTCCT 1680
537 ACAGTAGCAA CTCCTACGCA CTATGGGTAT CAAGGTACTT GGGGAATGAC TTGGGTTGAT 1740
538 GATACCGCAA GCACTCCAAA GACTAAGACA GCGACATTAG CTTGGACCAA TACAGGCTAC 1800
539 CTTCCGAATC CTGAGCGTCA AGGACCTTTA GTTCCTAATA GCCTTTGGGG ATCTTTTTCA 1860
540 GACATCCAAG CGATTCAAGG TGTCATAGAG AGAAGTGCTT TGACTCTTTG TTCAGATCGA 1920
541 GGCTTCTGGG CTGCGGGAGT CGCCAATTTC TTAGATAAAG ATAAGAAAGG GGAAAAACGC 1980
542 AAATACCGTC ATAAATCTGG TGGATATGCT ATCGGAGGTG CAGCGCAAAC TTGTTCTGAA 2040
543 AACTTAATTA GCTTTGCCTT TTGCCAACTC TTTGGTAGCG ATAAAGATTT CTTAGTCGCT 2100
544 AAAAATCATA CTGATACCTA TGCAGGAGCC TTCTATATCC AACACATTAC AGAATGTAGT 2160
545 GGGTTCATAG GTTGTCTCTT AGATAAACTT CCTGGCTCTT GGAGTCATAA ACCCCTCGTT 2220
546 TTAGAAGGGC AGCTCGCTTA TAGCCACGTC AGTAATGATC TGAAGACAAA GTATACTGCG 2280
547 TATCCTGAGG TGAAAGGTTC TTGGGGGAAT AATGCTTTTA ACATGATGTT GGGAGCTTCT 2340
548 TCTCATTCTT ATCCTGAATA CCTGCATTGT TTTGATACCT ATGCTCCATA CATCAAACTG 2400
549 AATCTGACCT ATATACGTCA GGACAGCTTC TCGGAGAAAG GTACAGAAGG AAGATCTTTT 2460
550 GATGACAGCA ACCTCTTCAA TTTATCTTTG CCTATAGGGG TGAAGTTTGA GAAGTTCTCT 2520
551 GATTGTAATG ACTTTTCTTA TGATCTGACT TTATCCTATG TTCCTGATCT TATCCGCAAT 2580
552 GATCCCAAAT GCACTACAGC ACTTGTAATC AGCGGAGCCT CTTGGGAAAC TTATGCCAAT 2640
553 AACTTAGCAC GACAGGCCTT GCAAGTGCGT GCAGGCAGTC ACTACGCCTT CTCTCCTATG 2700
554 TTTGAAGTGC TCGGCCAGTT TGTCTTTGAA GTTCGTGGAT CCTCACGGAT TTATAATGTA 2760
555 GATCTTGGGG GTAAGTTCCA ATTCTAGGAG CGTCTCTCAT GTCTCAGAAA TTCTG 2815
743 (2) INFORMATION FOR SEQ ID NO: 5:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,677

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Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3052 base pairs → see p. 4
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGCGATTTT CGCTCTGCGG ATTTCCTCTA GTTTTTTCTT TAACATTGCT CTCAGTCTTC 60
GACACTTCTT TGAGTGCTAC TACGATTTCT TTAACCCCAG AAGATAGTTT TCATGGAGAT 120
AGTCAGAATG CAGAACGTTC TTATAATGTT CAAGCTGGGG ATGTCTATAG CCTTACTGGT 180
GATGTCTCAA TATCTAACGT CGATAACTCT GCATTAAATA AAGCCTGCTT CAATGTGACC 240
TCAGGAAGTG TGACGTTCGC AGGAAATCAT CATGGGTTAT ATTTTAATAA TATTTCCTCA 300
GGAACTACAA AGGAAGGGGC TGTACTTTGT TGCCAAGATC CTCAAGCAAC GGCACGTTTT 360
TCTGGGTTCT CCACGCTCTC TTTTATTCAG AGCCCCGGAG ATATTAAAGA ACAGGGATGT 420
CTCTATTCAA AAAATGCACT TATGCTCTTA AACAATTATG TAGTGCGTTT TGAACAAAAC 480
CAAAGTAAGA CTAAAGGCGG AGCTATTAGT GGGGCGAATG TTACTATAGT AGGCAACTAC 540
GATTCCGTCT CTTTCTATCA GAATGCAGCC ACTTTTGGAG GTGCTATCCA TTCTTCAGGT 600
CCCCTACAGA TTGCAGTAAA TCAGGCAGAG ATAAGATTTG CACAAAATAC TGCCAAGAAT 660
GGTTCTGGAG GGGCTTTGTA CTCCGATGGT GATATTGATA TTGATCAGAA TGCTTATGTT 720
CTATTTCGAG AAAATGAGGC ATTGACTACT GCTATAGGTA AGGGAGGGGC TGTCTGTTGT 780
CTTCCCACTT CAGGAAGTAG TACTCCAGTT CCTATTGTGA CTTTCTCTGA CAATAAACAG 840
TTAGTCTTTG AAAGAAACCA TTCCATAATG GGTGGCGGAG CCATTTATGC TAGGAAACTT 900
AGCATCTCTT CAGGAGGTCC TACTCTATTT ATCAATAATA TATCATATGC AAATTCGCAA 960
AATTTAGGTG GAGCTATTGC CATTGATACT GGAGGGGAGA TCAGTTTATC AGCAGAGAAA 1020
GGAACAATTA CATTCCAAGG AAACCGGACG AGCTTACCGT TTTTGAATGG CATCCATCTT 1080
TTACAAAATG CTAAATTCCT GAAATTACAG GCGAGAAATG GATGCTCTAT AGAATTTTAT 1140
GATCCTATTA CTTCTGAAGC AGATGGGTCT ACCCAATTGA ATATCAACGG AGATCCTAAA 1200
AATAAAGAGT ACACAGGGAC CATACTCTTT TCTGGAGAAA AGAGTCTAGC AAACGATCCT 1260
AGGGATTTTA AATCTACAAT CCCTCAGAAC GTCAACCTGT CTGCAGGATA CTTAGTTATT 1320
AAAGAGGGGG CCGAAGTCAC AGTTTCAAAA TTCACGCAGT CTCCAGGATC GCATTTAGTT 1380
TTAGATTTAG GAACCAAACT GATAGCCTCT AAGGAAGACA TTGCCATCAC AGGCCTCGCG 1440
ATAGATATAG ATAGCTTAAG CTCATCCTCA ACAGCAGCTG TTATTAAAGC AAACACCGCA 1500
AATAAACAGA TATCCGTGAC GGACTCTATA GAACTTATCT CGCCTACTGG CAATGCCTAT 1560
GAAGATCTCA GAATGAGAAA TTCACAGACG TTCCCTCTGC TCTCTTTAGA GCCTGGAGCC 1620
GGGGGTAGTG TGACTGTAAC TGCTGGAGAT TTCCTACCGG TAAGTCCCCA TTATGGTTTT 1680
CAAGGCAATT GGAAATTAGC TTGGACAGGA ACTGGAAACA AAGTTGGAGA ATTCTTCTGG 1740
GATAAAATAA ATTATAAGCC TAGACCTGAA AAAGAAGGAA ATTTAGTTCC TAATATCTTG 1800
TGGGGGAATG CTGTAAATGT CAGATCCTTA ATGCAGGTTC AAGAGACCCA TGCATCGAGC 1860
TTACAGACAG ATCGAGGGCT GTGGATCGAT GGAATTGGGA ATTTCTTCCA TGTATCTGCC 1920
TCCGAAGACA ATATAAGGTA CCGTCATAAC AGCGGTGGAT ATGTTCTATC TGTAAATAAT 1980
GAGATCACAC CTAAGCACTA TACTTCGATG GCATTTTCCC AACTCTTTAG TAGAGACAAG 2040
GACTATGCGG TTTCCAACAA CGAATACAGA ATGTATTTAG GATCGTATCT CTATCAATAT 2100
ACAACCTCCC TAGGGAATAT TTTCCGTTAT GCTTCGCGTA ACCCTAATGT AAACGTCGGG 2160
ATTCTCTCAA GAAGGTTTCT TCAAAATCCT CTTATGATTT TTCATTTTTT GTGTGCTTAT 2220
GGTCATGCCA CCAATGATAT GAAAACAGAC TACGCAAATT TCCCTATGGT GAAAAACAGC 2280
TGGAGAAACA ATTGTTGGGC TATAGAGTGC GGAGGGAGCA TGCCTCTATT GGTATTTGAG 2340
AACGGAAGAC TTTTCCAAGG TGCCATCCCA TTTATGAAAC TACAATTAGT TTATGCTTAT 2400
CAGGGAGATT TCAAAGAGAC GACTGCAGAT GGCCGTAGAT TTAGTAATGG GAGTTTAACA 2460
TCGATTTCTG TACCTCTAGG CATACGCTTT GAGAAGCTGG CACTTTCTCA GGATGTACTC 2520

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Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I44667.7.raw

```
797 TATGACTTTA GTTTCTCCTA TATTCCTGAT ATTTTCCGTA AGGATCCCTC ATGTGAAGCT   2580
798 GCTCTGGTGA TTAGCGGAGA CTCCTGGCTT GTTCCGGCAG CACACGTATC AAGACATGCT   2640
799 TTTGTAGGGA GTGGAACGGG TCGGTATCAC TTTAACGACT ATACTGAGCT CTTATGTCGA   2700
800 GGAAGTATAG AATGCCGCCC CCATGCTAGG AATTATAATA TAAACTGTGG AAGCAAATTT   2760
801 CGTTTTTAGA AGGTTTCCAT TGCCTGTGTG GTTCCGGATC TTAACTATAA ATCCTGGACT   2820
802 ATGGATCATA GGCATTGGGT TTCTCGAACT TGTGTGGAGA ATAACGACAT TTTATATGCA   2880
803 TAACGGAATA CTCGTATCAC CTCAGCCCCT AGAGACATTC TTTAGGGGTT CTTTATTTGT   2940
804 CTAAACTTCG TATTTTATCG AGAATCCTTT ACGTTCTTGG TTTGCTTGTC TCCGAGGAGT   3000
E--> 805 TCTCTAACGA ATCATAGGGA TTCCAGGGTT CTGTTCCTTG AGTCCTTTGG A       3052
2597 (2) INFORMATION FOR SEQ ID NO: 24:
2599      (i) SEQUENCE CHARACTERISTICS:
2600           (A) LENGTH: 946 amino acids
2601           (B) TYPE: amino acid
2602           (C) STRANDEDNESS: single
2603           (D) TOPOLOGY: linear
2605      (ii) MOLECULE TYPE: peptide
2607      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
2609 Met Lys Thr Ser Val Ser Met Leu Leu Ala Leu Leu Cys Ser Gly Ala
2610   1               5                  10                  15
2612 Ser Ser Ile Val Leu His Ala Ala Thr Thr Pro Leu Asn Pro Glu Asp
2613              20                  25                  30
2615  Gly Phe Ile Gly Glu Gly Asn Thr Asn Thr Phe Ser Pro Lys Ser Thr
2616          35                  40                  45
2618 Thr Asp Ala Ala Gly Thr Thr Tyr Ser Leu Thr Gly Glu Val Leu Phe
2619      50                  55                  60
2621 Ile Asp Pro Gly Lys Gly Gly Ser Ile Thr Gly Thr Cys Phe Val Glu
2622  65                  70                  75                  80
2624 Thr Ala Gly Asp Leu Thr Phe Leu Gly Asn Gly Asn Thr Leu Lys Phe
2625                  85                  90                  95
2627 Leu Ser Val Asp Ala Gly Ala Asn Ile Ala Val Ala His Val Gln Gly
2628              100                 105                 110
2630 Ser Lys Asn Leu Ser Phe Thr Asp Phe Leu Ser Leu Val Ile Thr Glu
2631          115                 120                 125
2633 Ser Pro Lys Ser Ala Val Ser Thr Gly Lys Gly Ser Leu Val Ser Ser
2634      130                 135                 140
2636 Gly Ala Val Gln Leu Gln Asp Ile Asn Thr Leu Val Leu Thr Ser Asn
2637 145                 150                 155                 160
2639 Ala Ser Val Glu Asp Gly Gly Val Ile Lys Gly Asn Ser Cys Leu Ile
2640                 165                 170                 175
2642 Gln Gly Ile Lys Asn Ser Ala Ile Phe Gly Gln Asn Thr Ser Ser Lys
2643              180                 185                 190
2645 Lys Gly Gly Ala Ile Ser Thr Thr Gln Gly Leu Thr Ile Glu Asn Asn
2646          195                 200                 205
2648 Leu Gly Thr Leu Lys Phe Asn Glu Asn Lys Ala Val Thr Ser Gly Gly
2649      210                 215                 220
2651 Ala Leu Asp Leu Gly Ala Ala Ser Thr Phe Thr Ala Asn His Glu Leu
2652 225                 230                 235                 240
2654 Ile Phe Ser Gln Asn Lys Thr Ser Gly Asn Ala Ala Asn Gly Gly Ala
2655                 245                 250                 255
```

Number of bases conflict, 3052 listed, 3051 found.

→ See p. 6

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Input Set : A:\Birkell.txt
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```
2657 Ile Asn Cys Ser Gly Asp Leu Thr Phe Thr Asp Asn Thr Ser Leu Leu
2658                 260                 265                 270
2660 Leu Gln Glu Asn Ser Thr Met Gln Asp Gly Gly Ala Leu Cys Ser Thr
2661         275                 280                 285
2663 Gly Thr Ile Ser Ile Thr Gly Ser Asp Ser Ile Asn Val Ile Gly Asn
2664     290                 295                 300
2666 Thr Ser Gly Gln Lys Gly Gly Ala Ile Ser Ala Ala Ser Leu Lys Ile
2667 305                 310                 315                 320
2669 Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His
2670                 325                 330                 335
2672 Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu
2673             340                 345                 350
2675 Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val
2676         355                 360                 365
2678 Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu
2679     370                 375                 380
2681 Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala
2682 385                 390                 395                 400
2684 Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp
2685                 405                 410                 415
2687 Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser
2688             420                 425                 430
2690 Ile Val Phe Ser Gly Glu Arg Leu Ser Thr Ala Glu Ala Ile Ala Glu
2691         435                 440                 445
2693 Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser
2694     450                 455                 460
2696 Leu Glu Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln
2697 465                 470                 475                 480
2699 Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu Gln Ala
2700                 485                 490                 495
2702 Ser Thr Glu Asp Ile Val Ile Thr Asn Ser Ser Ile Asn Ala Asp Thr
2703             500                 505                 510
2705 Ile Tyr Gly Lys Asn Pro Ile Asn Ile Val Ala Ser Ala Ala Asn Lys
2706         515                 520                 525
2708 Asn Ile Thr Leu Thr Gly Thr Leu Ala Leu Val Asn Ala Asp Gly Ala
2709     530                 535                 540
2711 Leu Tyr Glu Asn His Thr Leu Gln Asp Ser Gln Asp Tyr Ser Phe Val
2712 545                 550                 555                 560
2714 Lys Leu Ser Pro Gly Ala Gly Gly Thr Ile Ile Thr Gln Asp Ala Ser
2715                 565                 570                 575
2717 Gln Lys Leu Leu Glu Val Ala Pro Ser Arg Pro His Tyr Gly Tyr Gln
2718             580                 585                 590
2720 Gly His Trp Asn Val Gln Val Ile Pro Gly Thr Gly Thr Gln Pro Ser
2721         595                 600                 605
2723 Gln Ala Asn Leu Glu Trp Val Arg Thr Gly Tyr Leu Pro Asn Pro Glu
2724     610                 615                 620
2726 Arg Gln Gly Phe Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Val Asp
2727 625                 630                 635                 640
2729 Gln Arg Ala Ile Gln Glu Ile Met Val Asn Ser Ser Gln Ile Leu Cys
```

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```
                645                 650                 655
Gln Glu Arg Gly Val Trp Gly Ala Gly Ile Ala Asn Phe Leu His Arg
            660                 665                 670
Asp Lys Ile Asn Glu His Gly Tyr Arg His Ser Gly Val Gly Tyr Leu
        675                 680                 685
Val Gly Val Gly Thr His Ala Phe Ser Asp Ala Thr Ile Asn Ala Ala
    690                 695                 700
Phe Cys Gln Leu Phe Ser Arg Asp Lys Asp Tyr Val Val Ser Lys Asn
705                 710                 715                 720
His Gly Thr Ser Tyr Ser Gly Val Val Phe Leu Glu Asp Thr Leu Glu
                725                 730                 735
Phe Arg Ser Pro Gln Gly Phe Tyr Thr Asp Ser Ser Ser Glu Ala Cys
            740                 745                 750
Cys Asn Gln Val Val Thr Ile Asp Met Gln Leu Ser Tyr Ser His Arg
        755                 760                 765
Asn Asn Asp Met Lys Thr Lys Tyr Thr Thr Tyr Pro Glu Ala Gln Gly
    770                 775                 780
Ser Trp Ala Asn Asp Val Phe Gly Leu Glu Phe Gly Ala Thr Thr Tyr
785                 790                 795                 800
Tyr Tyr Pro Asn Ser Thr Phe Leu Phe Asp Tyr Tyr Ser Pro Phe Leu
                805                 810                 815
Arg Leu Gln Cys Thr Tyr Ala His Gln Glu Asp Phe Lys Glu Thr Gly
            820                 825                 830
Gly Glu Val Arg His Phe Thr Ser Gly Asp Leu Phe Asn Leu Ala Val
        835                 840                 845
Pro Ile Gly Val Lys Phe Glu Arg Phe Ser Asp Cys Lys Arg Gly Ser
    850                 855                 860
Tyr Glu Leu Thr Leu Ala Tyr Val Pro Asp Val Ile Arg Lys Asp Pro
865                 870                 875                 880
Lys Ser Thr Ala Thr Leu Ala Ser Gly Ala Thr Trp Ser Thr His Gly
                885                 890                 895
Asn Asn Leu Ser Arg Gln Gly Leu Gln Leu Arg Leu Gly Asn His Cys
            900                 905                 910
Leu Ile Asn Pro Gly Ile Glu Val Phe Ser His Gly Ala Ile Glu Leu
        915                 920                 925
Arg Gly Ser Ser Arg Asn Tyr Asn Ile Asn Leu Gly Gly Lys Tyr Arg
    930                 935                 940
Phe
E--> 945
```

945 amino acids found, 946 listed as length.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/446,677

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Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:38 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:510 M:320 E: (1) Wrong Nucleic Acid Designator, 2
L:805 M:254 E: No. of Bases conflict, Input:3052 Counted:3051 SEQ:5
L:805 M:204 E: No. of Bases differ, LENGTH:Input:3052 Counted:3051 SEQ:5
L:2454 M:220 C: Keyword misspelled or invalid format, [(ii) MOLECULE TYPE:]
L:2787 M:203 E: No. of Seq. differs, LENGTH:Input:946 Found:945 SEQ:24